

GenCore version 5.1.3
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Om protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 14:7051 Seconds

Title: US-09-972-268-10

Perfect score: 2711

Sequence: 1 MARRPGPSPLCIGGGKAQLS.....KHHONNDPKKVYIDPREHYV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 9
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
|------------|--------|--------------|--------------------------|---|
| 1 | 1173.5 | 43.3 | 407 | 2 T08732 hypothetical protein DKFP566B0846.1 - human (fragment) |
| 2 | 565.5 | 20.9 | 518 | 2 JC0434 Homo sapiens (man) |
| 3 | 540 | 19.9 | 530 | 2 A53437 poliovirus receptor |
| 4 | 527 | 19.4 | 538 | 2 168093 PRB2 delta - human |
| 5 | 467 | 17.6 | 467 | 1 HLMSP3 poliovirus receptor |
| 6 | 455 | 16.8 | 478 | 2 153960 PRB2 alpha - human |
| 7 | 418 | 15.4 | 392 | 2 B44194 poliovirus receptor |
| 8 | 418 | 15.4 | 417 | 2 A44194 poliovirus receptor |
| 9 | 402 | 14.8 | 392 | 1 RWHPD poliovirus receptor |
| 10 | 402 | 14.8 | 417 | 1 RWHPD poliovirus receptor |
| 11 | 326.5 | 12.6 | 416 | 2 A54017 colon carcinoma-as irregular chiasm C |
| 12 | 229.5 | 8.5 | 764 | 2 A49448 perlecan precursor |
| 13 | 204.5 | 7.2 | 4391 | 2 A38096 hypothetical prote |
| 14 | 196.5 | 7.2 | 5175 | 2 T20992 hemifascin precursor |
| 15 | 196.5 | 7.2 | 5198 | 2 T43290 ox-2 membrane glycoprotein |
| 16 | 187.5 | 6.9 | 274 | 2 A47639 melin-associated |
| 17 | 181.5 | 6.7 | 1896 | 2 T08851 melin-associated |
| 18 | 178 | 6.6 | 588 | 2 JH0506 elastic titin - hu |
| 19 | 178 | 6.6 | 588 | 2 A45254 surface glycoprote |
| 20 | 177.5 | 6.5 | 853 | 1 IUBONC neural cell adhesi |
| 21 | 177 | 6.5 | 626 | 1 A61084 melin-associated |
| 22 | 177 | 6.5 | 637 | 2 B33785 melin-associated |
| 23 | 176 | 6.5 | 7962 | 2 138346 elastic titin - hu |
| 24 | 175 | 6.5 | 582 | 1 ENRTS melin-associated |
| 25 | 175 | 6.5 | 626 | 1 BNRT3 gial cell membran |
| 26 | 174 | 6.4 | 1091 | 2 A58532 heparan sulfate pr |
| 27 | 172.5 | 6.4 | 31822 coxsackie- and ade | |
| 28 | 170.5 | 6.3 | 365 | 2 JC7780 B-cell adhesion pr |
| 29 | 164.5 | 6.1 | 847 | 2 JH0371 |

| | | | | |
|----|-------|-----|------|-----------------------------|
| 30 | 162.5 | 6.0 | 278 | 1 TDRTDX OX-2 membrane glyc |
| 31 | 162.5 | 6.0 | 858 | 1 IJRTNC neural cell adhesi |
| 32 | 162 | 6.0 | 587 | 2 JH0464 TN-GRASP Precursor |
| 33 | 162 | 6.0 | 761 | 1 IJHNG neural cell adhesi |
| 34 | 162 | 6.0 | 765 | 2 C42652 cell adhesion mole |
| 35 | 162 | 6.0 | 812 | 2 B42532 cell adhesion mole |
| 36 | 162 | 6.0 | 932 | 2 A42632 vascular cell adhe |
| 37 | 161.5 | 6.0 | 739 | 2 JN0811 carcirembryonic a |
| 38 | 160.5 | 5.9 | 702 | 2 A36319 neural cell adhesi |
| 39 | 160 | 5.9 | 725 | 1 JPMENG SHP substrate-1 pr |
| 40 | 157 | 5.8 | 509 | 2 JC5588 neural cell adhesi |
| 41 | 157 | 5.8 | 1091 | 1 IJCRNL cell surface glyco |
| 42 | 155 | 5.8 | 646 | 2 J38049 SIP substrate-1 pr |
| 43 | 155 | 5.7 | 513 | 2 JC5589 durtl protein - mo |
| 44 | 154 | 5.7 | 1612 | 2 T30805 kinase-like protei |
| 45 | 153.5 | 5.7 | 1051 | 2 A39712 |

ALIGNMENTS

RESULT 1
T08732 hypothetical protein DKFP566B0846.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 11-Jun-1999 #Sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C.Accession: T08732
R.Ottewaalder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Reduced: 1;407 <OPT>
A;Cross-references: EMBL:AU50071
A;Experimental source: fetal kidney; clone DKZP566B0846
C;Genetics:
A;Note: DKZP566B0846.1

Query Match Similarity 43.3%; Score 1173.5; DB 2; Length 407;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

Db 143 SGKTCIKAVTFQDGNQASSTTVTFVTPVSKLKDPSLDGNETWMAICATGKPV 202
1 SGKTCIKAVTFQDGNQASSTTVTFVTPVSKLKDPSLDGNETWMAICATGKPV 60
Db 203 HIDMEGDGEMSTTSFPPNETATTTISOCYKUPTPARGERTCIVKHPALEKDIRYSFI 262
1 HIDMEGDGEMSTTSFPPNETATTTISOCYKUPTPARGERTCIVKHPALEKDIRYSFI 120
Db 61 HIDMEGDGEMSTTSFPPNETATTTISOCYKUPTPARGERTCIVKHPALEKDIRYSFI 120
QY 263 UDQYAPESVUTGDDANWFGKVKUNLKNADANPPFKSVWRLDQMPDGILASDNTL 322
Db 121 UDQYAPESVUTGDDANWFGKVKUNLKNADANPPFKSVWRLDQMPDGILASDNTL 180
QY 323 HFVPLTENSYCVYIICVTKNSLGRSRDKQVYIISYP----- 359
Db 181 HFVPLTENSYCVYIICVTKNSLGRSRDKQVYIISYP----- 240
OY 360 -----FQTSSIAVAGAVIAGVIAITATTFVUTVLTPIKK--RPSLTDKV 403
Db 241 ERKULPFPLSLTAKTODITATIASVUGGLPVLVSLAGFCYRARRFRGIVFAK 300
OY 404 IDLPRT-----KEPPVLEERSPPRPOKDFQPFHL--PLQTOFKEREVG 446
Db 301 Y-LIPSDMOKESQDVLQDDELPYPSVVKKENKUPVNLLRKDYLSEPEKTQW---N 354
QY 447 NLQISGNGNSRSFDDYDENVG 468
Db 355 NVENLNRP-ERPMDDYEDLKG 375

RESULT 2
J4024

| Copyright (c) 1993 - 2002 Compugen Ltd. | GenCore version 5.1.3 | | |
|--|----------------------------------|--------------------------|---|
| OM protein - protein search, using SW model. | | | |
| Run on: December 15, 2002, 09:04:27 ; Search time 14.7051 Seconds | (without alignments) | | |
| Title: US-09-972-268-12 | 334.117 Million cell updates/sec | | |
| Perfect score: 2707 | | | |
| Sequence: 1 MARTIRPSPICPGGKGQLS.....KHEQNNDPKRYVDPREHYV 510 | | | |
| Scoring table: BLOSUM62 | | | |
| Searched: GapOp 10.0 , GapExt 0.5 | | | |
| number of hits satisfying chosen parameters: | 283224 | | |
| Minimum DB seq length: 0 | | | |
| Post-processing: Minimum Match 0 % | | | |
| Database : PIR_71* | Maximum Match 100% | | |
| 1: pi1;* | Listing first 45 summaries | | |
| 2: pi2;* | | | |
| 3: pi3;* | | | |
| 4: pi4;* | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | |
| SUMMARIES | | | |
| Result No. | Score | Query Match Length DB ID | Description |
| 1 | 1173.5 | 43.4 407 2 T09732 | hypothetical protein DKFP566B0046.1 - human (fragment) |
| 2 | 555.5 | 20.9 518 2 JC4024 | C;Species: Homo Sapiens (man) |
| 3 | 540 | 19.9 530 2 A53437 | C;Accession: 11-Jun-1999 #sequence_revision 11-Jun-1999 |
| 4 | 527 | 19.5 538 2 I68093 | R;Owner/welder: B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiesmann, S. |
| 5 | 477 | 17.3 515 2 HMSP3 | submitted to the Protein Sequence Database, May 1999 |
| 6 | 455 | 16.8 478 2 I53960 | A;Reference number: 216474 |
| 7 | 418 | 15.4 392 2 B44194 | A;Accession: T09732 |
| 8 | 416 | 15.4 417 2 A44194 | A;Molecule type: mRNA |
| 9 | 402 | 14.9 392 1 RHHPUD | A;Residues: 1-407 <OTT> |
| 10 | 394 | 14.9 417 1 RHUPA | A;Cross-references: EMBL:AL050071 |
| 11 | 326.5 | 12.1 416 2 A54017 | A;Experimental source: fetal kidney; clone DKFP566B00846.1 |
| 12 | 239.5 | 8.5 764 2 A49448 | C;Genetic: |
| 13 | 205.5 | 7.6 4391 2 A38096 | A;Note: DKFP566B00846.1 |
| 14 | 196.5 | 7.3 5125 2 T20992 | Query Match Similarity 43.4%; Score 1173.5/-DB 2; length 407; |
| 15 | 196.5 | 7.3 5198 2 T43290 | Best Local Similarity 62.8%; Pred. No. 3.9e-78; Mismatches 51; Indels 63; Gaps 7; |
| 16 | 187.5 | 6.9 274 2 A47639 | Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7; |
| 17 | 181.5 | 6.7 1896 2 T08851 | Db 143 SGKVICKAVTPIGLQASSTTVVLPVPTVLSIKPDSIDGENETPAACIATNGKVA 202 |
| 18 | 178.5 | 6.6 3707 2 S18252 | Db 1 SGKVICKAVTPIGLQASSTTVVLPVPTVLSIKPDSIDGENETPAACIATNGKVA 60 |
| 19 | 178 | 6.6 588 2 JR0506 | QY 203 HIDEKGDGEMESTTSFENNTATISQVQLPPTPRARERRITCVVHPALBKDQYRPI 262 |
| 20 | 178 | 6.6 589 2 A45254 | Db 61 HIDEGDGEMESTTSFENNTATISQVQLPPTPRARERRITCVVHPALBKDQYRPI 120 |
| 21 | 177.5 | 6.6 853 1 -TUBONC | QY 263 LDQTYADAEVSIVTGQWVGRKGKVNCKMDANPPPKSVMSRLDCQWPGGLASDNTL 322 |
| 22 | 177 | 6.5 626 1 A61084 | Db 121 LDQTYADAEVSIVTGQWVGRKGKVNCKMDANPPPKSVMSRLDCQWPGGLASDNTL 180 |
| 23 | 177 | 6.5 637 2 B33785 | QY 323 HFVPLIPFTNPGVYVTKVNTLGQRSDQKVYV1SDVP----- 359 |
| 24 | 176 | 6.5 7962 2 I38346 | Db 181 HFVPLIPFTNPGVYVTKVNTLGQRSDQKVYV1SDVP----- 240 |
| 25 | 175 | 6.5 582 1 BMR73S | QY 360 -----PKQFSSIAVAGAVIGAVIALFIAIFVFTVLUTPRKE--RSYLPDKV 403 |
| 26 | 175 | 6.5 626 1 BMR73 | Db 241 EPKULPFLSLATIATKDFATIASVGGALPITVSYLAGFCRRRTFRGDYAFN 300 |
| 27 | 174 | 6.4 1091 2 AS8532 | QY 404 IDUPTH-----KPPPLKERSSPPLPKOLOPQEHL--PLTOFFGEREVG 446 |
| 28 | 170.5 | 6.3 365 2 JC7780 | Db 301 Y-IIPSPDMQKSOIOWLQDLPDPVSKKENKNPKVNNLIRDYLFEPKTQ---N 354 |
| 29 | 164.5 | 6.1 847 2 JH0371 | QY 447 NLQHSNGLNSGRSPDVEDENPVG 468 |
| | | | Db 355 NVMNLNR-ERPMDVYEDLQG 375 |
| ALIGNMENTS | | | |
| RESULT 1 | | | |
| T09732 | | | |
| hypothetical protein DKFP566B0046.1 - human (fragment) | | | |
| C;Species: Homo Sapiens (man) | | | |
| C;Accession: 11-Jun-1999 #sequence_revision 11-Jun-1999 | | | |
| R;Owner/welder: B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiesmann, S. | | | |
| submitted to the Protein Sequence Database, May 1999 | | | |
| A;Reference number: 216474 | | | |
| A;Accession: T09732 | | | |
| A;Molecule type: mRNA | | | |
| A;Residues: 1-407 <OTT> | | | |
| A;Cross-references: EMBL:AL050071 | | | |
| A;Experimental source: fetal kidney; clone DKFP566B00846.1 | | | |
| C;Genetic: | | | |
| A;Note: DKFP566B00846.1 | | | |
| Query Match Similarity 43.4%; Score 1173.5/-DB 2; length 407; | | | |
| Best Local Similarity 62.8%; Pred. No. 3.9e-78; Mismatches 51; Indels 63; Gaps 7; | | | |
| Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7; | | | |
| Db 143 SGKVICKAVTPIGLQASSTTVVLPVPTVLSIKPDSIDGENETPAACIATNGKVA 202 | | | |
| Db 1 SGKVICKAVTPIGLQASSTTVVLPVPTVLSIKPDSIDGENETPAACIATNGKVA 60 | | | |
| QY 203 HIDEKGDGEMESTTSFENNTATISQVQLPPTPRARERRITCVVHPALBKDQYRPI 262 | | | |
| Db 61 HIDEGDGEMESTTSFENNTATISQVQLPPTPRARERRITCVVHPALBKDQYRPI 120 | | | |
| QY 263 LDQTYADAEVSIVTGQWVGRKGKVNCKMDANPPPKSVMSRLDCQWPGGLASDNTL 322 | | | |
| Db 121 LDQTYADAEVSIVTGQWVGRKGKVNCKMDANPPPKSVMSRLDCQWPGGLASDNTL 180 | | | |
| QY 323 HFVPLIPFTNPGVYVTKVNTLGQRSDQKVYV1SDVP----- 359 | | | |
| Db 181 HFVPLIPFTNPGVYVTKVNTLGQRSDQKVYV1SDVP----- 240 | | | |
| QY 360 -----PKQFSSIAVAGAVIGAVIALFIAIFVFTVLUTPRKE--RSYLPDKV 403 | | | |
| Db 241 EPKULPFLSLATIATKDFATIASVGGALPITVSYLAGFCRRRTFRGDYAFN 300 | | | |
| QY 404 IDUPTH-----KPPPLKERSSPPLPKOLOPQEHL--PLTOFFGEREVG 446 | | | |
| Db 301 Y-IIPSPDMQKSOIOWLQDLPDPVSKKENKNPKVNNLIRDYLFEPKTQ---N 354 | | | |
| QY 447 NLQHSNGLNSGRSPDVEDENPVG 468 | | | |
| Db 355 NVMNLNR-ERPMDVYEDLQG 375 | | | |
| RESULT 2 | | | |
| JC4024 | | | |



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Om protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 15.6278 Seconds

Title: US-09-972-268-2
Perfect score: 2866
Sequence: I SPCPGCKHQLSASLIGA. EDDLVSHVDGSVISREWWV 542

Scoring table: Blosum62
Gapp 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
1 number of hits satisfying chosen parameters: 283224

Maximum DB seq length: 0
Maximum DB length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR-73:
1: Pir1:
2: Pir2:
3: Pir3:
4: Pir4:
5: Pir5:
6: Pir6:
7: Pir7:
8: Pir8:
9: Pir9:
10: Pir10:
11: Pir11:
12: Pir12:
13: Pir13:
14: Pir14:
15: Pir15:
16: Pir16:
17: Pir17:
18: Pir18:
19: Pir19:
20: Pir20:
21: Pir21:
22: Pir22:
23: Pir23:
24: Pir24:
25: Pir25:
26: Pir26:
27: Pir27:
28: Pir28:
29: Pir29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|-----------|---|
| 1 | 2141 | 74.7 | 407 | T08732 | hypothetical protein DKFZp566B0046.1 - human (fragment) |
| 2 | 627 | 21.9 | 518 | JC024 | C;Species: Homo sapiens (man) |
| 3 | 494 | 17.2 | 467 | 1 HLMSP3 | C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999 |
| 4 | 470 | 16.4 | 530 | 2 A53437 | C;Accession: T08732 |
| 5 | 463.5 | 16.2 | 478 | 165967 | R;Ottewaelter, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. |
| 6 | 449.5 | 15.7 | 538 | 2 165903 | submitted to the Protein Sequence Database, May 1999 |
| 7 | 422.5 | 14.7 | 417 | 2 A41194 | A;Reference number: 216474 |
| 8 | 415.5 | 14.5 | 392 | 2 B44194 | A;Accession: T08732 |
| 9 | 390.5 | 13.6 | 392 | 1 RWHPUD | A;Molecule type: mRNA |
| 10 | 390.5 | 13.6 | 417 | 1 RWHPUPA | A;Cross-references: EMBL:AL050071 |
| 11 | 331.5 | 11.6 | 416 | 2 A5017 | A;Experimental source: fetal kidney: clone DKFZp566B0046.1 |
| 12 | 230.5 | 8.0 | 764 | 2 A44448 | C;Genetics: A;Note: DKFZp566B0046.1 |
| 13 | 215.5 | 7.5 | 4391 | 2 A3096 | Query 136 SAKVIAKAVTPPLAGNAGSSTTIVUPEPTVLSIKPGPSLQSGNTVAVICIAATGKVA 195 |
| 14 | 201 | 7.0 | 5175 | 2 T2992 | Db 1 SEKVIKAVAVTPPLAGNAGSSTTIVUPEPTVLSIKPGPSLQSGNTVAVICIAATGKVA 60 |
| 15 | 201 | 7.0 | 5198 | 2 T43290 | Qy 196 HITDWEGLGENESTTSPPNETATTTISQYKLPPTRANGRGRITCWPKHALEDIRVSPF 255 |
| 16 | 198 | 6.9 | 588 | 2 JH0506 | Db 61 HITDWEGLGENESTTSPPNETATTTISQYKLPPTRANGRGRITCWPKHALEDIRVSPF 120 |
| 17 | 194 | 6.8 | 588 | 2 A42254 | Qy 256 LDIQVAPAVTGTGDNWFGRKGSNLKCNADANPPFKSWRSLQDQMDGQASMTL 315 |
| 18 | 189 | 6.6 | 853 | 1 LTRONC | Db 121 LDIQVAPAVTGTGDNWFGRKGSNLKCNADANPPFKSWRSLQDQMDGQASMTL 180 |
| 19 | 187.5 | 6.5 | 274 | 2 A41639 | Qy 316 HFVPLTFNNSGVICKTNSLGQRSDOKITYSDPPTTILQPIYQWIRSTADIEPLAT 375 |
| 20 | 187.5 | 6.5 | 7962 | 2 T38346 | Db 181 HFVPLTFNNSGVICKTNSLGQRSDOKITYSDPPTTILQPIYQWIRSTADIEPLAT 240 |
| 21 | 182 | 6.4 | 587 | 2 JH0464 | Qy 376 EPRKLUPPPLSTATIKDTIATIASWVGALFLIVLVSAGIFCRRTFRGDFAKN 435 |
| 22 | 181.5 | 6.3 | 1895 | 2 T08851 | Db 241 EPRKLUPPPLSTATIKDTIATIASWVGALFLIVLVSAGIFCRRTFRGDFAKN 300 |
| 23 | 178.5 | 6.2 | 847 | 2 JH0371 | Qy 496 KERPMYDUDKNGKMEVSDHYDENEDDVSVDSVISREWWV 542 |
| 24 | 177 | 6.2 | 3707 | 2 S12525 | Db 361 RERPMYDUDKNGKMEVSDHYDENEDDVSVDSVISREWWV 407 |
| 25 | 174 | 6.1 | 858 | 1 TURUNC | Qy 436 YPPSPOMQESQIDWLOODEDLYPSDVKENKNPVPNLKDYLPPEKTMANVENLN 495 |
| 26 | 173.5 | 6.1 | 761 | 1 LHUNG | Db 301 YPPSPOMQESQIDWLOODEDLYPSDVKENKNPVPNLKDYLPPEKTMANVENLN 360 |
| 27 | 173 | 6.0 | 637 | 2 B33785 | Qy 496 KERPMYDUDKNGKMEVSDHYDENEDDVSVDSVISREWWV 542 |
| 28 | 172 | 6.0 | 513 | 2 JC5289 | Db 361 RERPMYDUDKNGKMEVSDHYDENEDDVSVDSVISREWWV 407 |
| 29 | 171.5 | 6.0 | 822 | 2 B49151 | Qy 496 KERPMYDUDKNGKMEVSDHYDENEDDVSVDSVISREWWV 542 |

RESULTS

ALIGNMENTS

| | | | | | |
|----|-------|-----|------|-----------|--------------------|
| 30 | 171 | 6.0 | 459 | 2 S23969 | cell-adhesion mole |
| 31 | 171 | 6.0 | 582 | 1 BRT3 | myelin-associated |
| 32 | 171 | 6.0 | 625 | 1 BRT3 | Bravo/N-CAM cell |
| 33 | 171 | 6.0 | 1259 | 2 A3425 | neural cell adhesi |
| 34 | 169.5 | 5.9 | 1091 | 1 ITCNHL | myelin-associated |
| 35 | 169 | 5.9 | 625 | 1 A51084 | cell adhesion mole |
| 36 | 168 | 5.9 | 765 | 2 C42632 | cell adhesion mole |
| 37 | 168 | 5.9 | 812 | 2 B42632 | cell adhesion mole |
| 38 | 168 | 5.9 | 932 | 2 A42632 | fibroblast growth |
| 39 | 165.5 | 5.8 | 822 | 2 S19947 | vascular cell adhe |
| 40 | 165 | 5.8 | 739 | 2 JN0581 | neural cell adhesi |
| 41 | 165 | 5.8 | 725 | 1 IJMSNL | neural cell adhesi |
| 42 | 165 | 5.8 | 1115 | 1 IJMSNL | T cell activation |
| 43 | 164.5 | 5.7 | 569 | 2 A46462 | biliary glycoprote |
| 44 | 164 | 5.7 | 521 | 2 JU1508 | biliary glycoprote |
| 45 | 163 | 5.7 | 458 | 1 RWMRSRL | biliary glycoprote |



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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 28.4142 Seconds
 (without alignments) 3930.349 Million cell updates/sec

Title: US-09-972-268-2

Perfect score: 2866

Sequence: 1 SPICPGGKQALSSASLIGA... EDDIIVSHVDSGVISRRERYV 542

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1

SPREBML 21:*

- 1: sp_archae:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_minic:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriop:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|--------|-------|--------------|-----------|-------------------------------|
| 1 | 2866 | 100.0 | 549 | 4 Q9WQS3 | Q9WQS3 homo sapien |
| 2 | 2700 | 94.2 | 549 | 1 Q9JLB9 | Q9JLB9 mus musculus |
| 3 | 256 | 92.7 | 549 | 1 Q9JLB9 | Q9JLB9 mus musculus |
| 4 | 2141 | 74.7 | 407 | 4 Q9Y412 | Q9Y412 homo sapien |
| 5 | 1793.5 | 62.6 | 510 | 1 Q9JLB8 | Q9JLB8 mus musculus |
| 6 | 1788.5 | 62.4 | 438 | 1 Q9JLB7 | Q9JLB7 mus musculus |
| 7 | 1629 | 56.8 | 304 | 4 Q9BV9 | Q9BV9 homo sapien |
| 8 | 544 | 19.0 | 510 | 4 Q96W8 | Q96W8 homo sapien |
| 9 | 543 | 18.9 | 510 | 4 Q96K5 | Q96K5 homo sapien |
| 10 | 542 | 18.9 | 101 | 4 Q8WU4 | Q8WU4 homo sapien |
| 11 | 534.5 | 18.5 | 295 | 1 Q8ERFS | Q8ERFS mesocricetus auratus |
| 12 | 528 | 18.4 | 298 | 6 Q9GJ74 | Q9GJ74 cercopithecus aethiops |
| 13 | 526 | 18.4 | 295 | 6 Q9GJ75 | Q9GJ75 bos taurus |
| 14 | 506 | 17.7 | 508 | 1 Q8R007 | Q8R007 mus musculus |
| 15 | 496 | 17.3 | 99 | 11 Q9CT80 | Q9CT80 mus musculus |
| 16 | 494 | 17.2 | 467 | 11 Q9IVT9 | Q9IVT9 mus musculus |

RESULT 1

| ID | Q9WQS3 | PRT: | 549 AA. |
|------------|--|--------------|---------|
| AC | Q9WQS3; | PRELIMINARY; | |
| DT | 01-OCT-2000 (TREMBLER. 15, Created) | | |
| DT | 01-OCT-2000 (TREMBLER. 15, Last sequence update) | | |
| DT | 01-DEC-2001 (TREMBLER. 19, Last annotation update) | | |
| DE | Nectin 3. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo. | | |
| NCBI TaxID | 9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G., | | |
| RA | Dubreuil P., Lopez M.; | | |
| RT | "Human nectin 3/rpr3: A novel member of the PVR/PRR/hectin family that interacts with afadin."; | | |
| RL | Gene 0.0-0.0001 | | |
| DR | EMBL; AF282871; AAP97597.1; -. | | |
| DR | InterPro; IPR003599; Ig_1. | | |
| DR | InterPro; IPR003600; Ig_MHC. | | |
| DR | InterPro; IPR003066; Ig_MHC. | | |
| DR | PIRn; PF00047; Ig_2. | | |
| DR | SMART; SMD0409; Ig_1. | | |
| DR | SMART; SMD0410; Ig_Like_1. | | |
| SQ | SEQUENCE: 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64; | | |
| DR | Query Match Similarity 100.0%; Score 2866; DB 4; Length 549; Best Local Similarity 100.0%; Pred. No. 4; 3e-217; Matches 542; Conservative 0; Mismatches 0; Gaps 0; Indels 0; | | |
| DR | Q9WQS3 | | |
| DR | 1 SPICPGGKQALSSASLIGA... EDDIIVSHVDSGVISRRERYV 60 | | |
| Db | 8 SPICPGGKQALSSASLIGA... EDDIIVSHVDSGVISRRERYV 67 | | |
| Qy | 61 AVWGVWSVSKCLTVEVNNTIQISWIKHKSSTQVAVHHPPOYGSVQSBYQSVLFRNYS 120 | | |
| Db | 68 AVWGVWSVSKCLTVEVNNTIQISWIKHKSSTQVAVHHPPOYGSVQSBYQSVLFRNYS 127 | | |

| | | | | | | | |
|-----------------|--|--|-----------------------------|------------------|---|--|-----------------------------|
| Qy | 121 | LNDATILNIGPSCKYICKAVTFFPLGNAQSSTTTVLEPTVSLIKGPDSLIDGNN | 180 | Qy | 61 | AWGKQNSKCLIEVNETITQISWEKINGKSSOTVAVHPOGRGSVQSEYQRVLFKNY | 120 |
| Db | 128 | LNDATILNIGPSCKYICKAVTFFPLGNAQSSTTTVLEPTVSLIKGPDSLIDGNN | 187 | Db | 69 | AWGKQNSKCLIEVNETITQISWEKINGKSSOTVAVHPOGRGSVQSEYQRVLFKNY | 127 |
| Qy | 181 | TVAACIAATGKPVAHIDWEGLGEMESTTSPNETATISQYKLFRFGRRTCV | 240 | Qy | 124 | INDATILHNGPSCKYICKAVTFFPLGNAQSSTTTVLEPTVSLIKGPDSLIDGNN | 180 |
| Db | 188 | TVAACIAATGKPVAHIDWEGLGEMESTTSPNETATISQYKLFRFGRRTCV | 247 | Db | 128 | INDATILHNGPSCKYICKAVTFFPLGNAQSSTTTVLEPTVSLIKGPDSLIDGNN | 187 |
| Qy | 241 | VKHPALEKDIRYSPILDIOVAAPEVSYTGDNMPVGRKGYNLKCNAANDANPPFKTSWSRL | 300 | Qy | 181 | TVAACIAATGKPVAHIDWEGLGEMESTTSPNETATISQYKLFRFGRRTCV | 240 |
| Db | 248 | VKHPALEKDIRYSPILDIOVAAPEVSYTGDNMPVGRKGYNLKCNAANDANPPFKTSWSRL | 307 | Db | 188 | TVAACIAATGKPVAHIDWEGLGEMESTTSPNETATISQYKLFRFGRRTCV | 247 |
| Qy | 301 | DGOWDGLIASDNTLHVPHLTENYSGYICKTNISQSDQKVYISDPPPTTTLQPT | 360 | Qy | 241 | VKHPALEKDIRYSPILDIOVAAPEVSYTGDNMPVGRKGYNLKCNAANDANPPFKTSWSRL | 300 |
| Db | 308 | DGOWDGLIASDNTLHVPHLTENYSGYICKTNISQSDQKVYISDPPPTTTLQPT | 367 | Db | 248 | VKHPALEKDIRYSPILDIOVAAPEVSYTGDNMPVGRKGYNLKCNAANDANPPFKTSWSRL | 307 |
| Qy | 361 | IQMHSSTADIEDATEBKCLFLPLSTAKDTIATIASVVGALPVLVSLAGIFC | 420 | Qy | 301 | DGOWDGLIASDNTLHVPHLTENYSGYICKTNISQSDQKVYISDPPPTTTLQPT | 360 |
| Db | 368 | IQMHSSTADIEDATEBKCLFLPLSTAKDTIATIASVVGALPVLVSLAGIFC | 427 | Db | 308 | DGOWDGLIASDNTLHVPHLTENYSGYICKTNISQSDQKVYISDPPPTTTLQPT | 367 |
| Qy | 421 | YRRRTRFGDYFAKNYIIPPSDMQKESQDQVLOQDLDSDYPSVSKKENKPNVLIRKDYL | 480 | Qy | 361 | IQMHSSTADIEDATEBKCLFLPLSTAKDTIATIASVVGALPVLVSLAGIFC | 420 |
| Db | 428 | YRRRTRFGDYFAKNYIIPPSDMQKESQDQVLOQDLDSDYPSVSKKENKPNVLIRKDYL | 487 | Db | 368 | YRRRTRFGDYFAKNYIIPPSDMQKESQDQVLOQDLDSDYPSVSKKENKPNVLIRKDYL | 427 |
| Qy | 481 | EPEPTQNNVENLNRFPERPMOYEDLKGWGMKTVUSDHYDENEDLVSHDGSVISRREW | 540 | Qy | 421 | YRRRTRFGDYFAKNYIIPPSDMQKESQDQVLOQDLDSDYPSVSKKENKPNVLIRKDYL | 480 |
| Db | 488 | EPEPTQNNVENLNRFPERPMOYEDLKGWGMKTVUSDHYDENEDDLVSHDGSVISRREW | 547 | Db | 428 | YRRRTRFGDYFAKNYIIPPSDMQKESQDQVLOQDLDSDYPSVSKKENKPNVLIRKDYL | 487 |
| Qy | 541 | YV 542 | | Qy | 481 | EPEPTQNNVENLNRFPERPMOYEDLKGWGMKTVUSDHYDENEDLVSHDGSVISRREW | 540 |
| Db | 548 | YV 549 | | Db | 488 | EPEPTQNNVENLNRFPERPMOYEDLKGWGMKTVUSDHYDENEDLVSHDGSVISRREW | 547 |
| Qy | 541 | YV 542 | | Qy | 541 | YV 542 | |
| Db | 548 | YV 549 | | Db | 548 | YV 549 | |
| RESULT 2 | | | | | | | |
| Q9JLB9 | | PRELIMINARY; | PRT; | 549 | AA. | | |
| AC | Q9JLB9, | | | | | | |
| ID | Q9JLB9, | | | | | | |
| DT | 01-OCT-2000 | (TrEMBL) | 15; Created) | Q9D006 | PRELIMINARY; | PRT; | 549 AA. |
| DT | 01-OCT-2000 | (TrEMBL) | 15; Last sequence update) | AC | | | |
| DB | 01-DEC-2001 | (TrEMBL) | 19; Last annotation update) | ID | Q9D006 | | |
| GN | PWNL3. | | | DT | 01-JUN-2001 | (TrEMBL) | 17; Created) |
| OS | Mus musculus (Mouse) | | | DT | 01-JUN-2001 | (TrEMBL) | 17; Last sequence update) |
| OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | DT | 01-DEC-2001 | (TrEMBL) | 19; Last annotation update) |
| OX | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | DE | 2610301B19RIK | protein. | |
| RN | [1] | | | GN | 2610301B19RIK | | |
| RP | SEQUENCE FROM N.A. | | | OS | Mus musculus (Mouse) | | |
| RX | MEDLINE=20020903; PubMed=10744716; | | | OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| RA | Setoh-Horikawa K., Nakanihi H., Takahashi K., Miyahara M., | | | OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| RA | RA | | | NCBI_TaxID=1090; | | | |
| RT | RA | | | RN | [1] | | |
| RT | RA | | | RP | SEQUENCE FROM N.A. | | |
| RT | RA | | | RC | SEQUENCE=C57BL/6J; TISSUE=EMBRYO; | | |
| RT | RA | | | RX | Medline=C57BL/6J; PubMed=11217851; | | |
| RT | RA | | | RA | Kawai J., Shinagawa A., Shibata R., Yoshino M., Itoh M., Ishii Y., | | |
| RT | RA | | | RA | Arakawa K., Hara M., Nishii K., Kiyosawa H., Konno H., Fukuda S., | | |
| RT | RA | | | RA | Aizawa K., Iizawa M., Nishii K., Kiyosawa H., Kondo S., Yamamoto I., | | |
| RT | RA | | | RA | Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., | | |
| RT | RA | | | RA | Kidota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., | | |
| RT | RA | | | RA | Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., | | |
| RT | RA | | | RA | Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pasole G., Quackenbush J., | | |
| RT | RA | | | RA | Schrimal L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., | | |
| RT | RA | | | RA | SAkai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., | | |
| RT | RA | | | RA | Blake J., Bottelli D., Boijunga N., Carninci P., de Bonaldo M.F., | | |
| RT | RA | | | RA | Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., | | |
| RT | RA | | | RA | Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., | | |
| RT | RA | | | RA | Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P., | | |
| RT | RA | | | RA | Nordone P., Ring B., Rinewald M., Rodriguez I., Sakamoto N., | | |
| RT | RA | | | RA | Sasaki H., Sato K., Schoenbach C., Saya T., Shabata Y., Storch K.-P., | | |
| RT | RA | | | RA | Suzuki H., Toyoi-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., | | |
| RT | RA | | | RA | Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S., | | |
| RT | RA | | | RA | Hayashizaki Y., | | |
| 8 | APLCGGKAQLSASSAGAILLQDPPLLLPILLFSRICGAGLGPVPHV | 67 | | | | | |

Query Match Score 2700; DB 11; Length 549;
 Best Local Similarity 93.2%; Pred. No. 204; 19; Mismatches 18; Indels 0; Gaps 0;
 Matches 505; Conservative 19; Nucleotides 19; NHC.
 PFAM: PF00047; ig_2
 SMART: SM0040; ig_1; SMART; SM00410; ig_1; SQ SEQUENCE 549 AA; 6583 MN: S492C9ABA72P185 CRC64;
 Q9JLB9; Score 2700; DB 11; Length 549;
 ID: Q9JLB9; AC: Q9JLB9; DT: 01-OCT-2000; PT: PRELIMINARY;
 PWNL3; Cell adhesion molecule neectin-3 alpha.
 OS: Mus musculus (Mouse)
 OC: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN: [1]
 RP: SEQUENCE FROM N.A.
 RX: MEDLINE=20020903; PubMed=10744716;
 RA: Setoh-Horikawa K., Nakanihi H., Takahashi K., Miyahara M.,
 RA: RA
 RT: Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
 RT: that shows homophilic and heterophilic cell-cell adhesion
 RT: activities.";
 RL: J. Biol. Chem. 275:10291-10299 (2000).
 DR: MGI:1930171; Pur13
 DR: AF195833; AAF63385; 1; -.
 DR: InterPro: IPR003599; 19; 19 like.
 DR: InterPro: IPR003600; 19; 19 like.
 DR: InterPro: IPR003006; 19; NHC.
 DR: Pfam: PF00047; ig_2
 DR: SMART: SM0040; ig_1; SMART; SM00410; ig_1; SQ SEQUENCE 549 AA; 6583 MN: S492C9ABA72P185 CRC64;
 Query Match Score 2700; DB 11; Length 549;
 Best Local Similarity 93.2%; Pred. No. 204; 19; Mismatches 18; Indels 0; Gaps 0;
 Matches 505; Conservative 19; Nucleotides 19; NHC.
 Q9JLB9; Score 2700; DB 11; Length 549;
 ID: Q9JLB9; AC: Q9JLB9; DT: 01-OCT-2000; PT: PRELIMINARY;
 PWNL3; Cell adhesion molecule neectin-3 alpha.
 OS: Mus musculus (Mouse)
 OC: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN: [1]
 RP: SEQUENCE FROM N.A.
 RC: SEQUENCE=C57BL/6J; TISSUE=EMBRYO;
 RX: Medline=C57BL/6J; PubMed=11217851;
 RA: Kawai J., Shinagawa A., Shibata R., Yoshino M., Itoh M., Ishii Y.,
 RA: Arakawa K., Hara M., Nishii K., Kiyosawa H., Konno H., Fukuda S.,
 RA: Aizawa K., Iizawa M., Nishii K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA: Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA: Kidota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA: Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA: Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pasole G., Quackenbush J.,
 RA: Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA: Blake J., Bottelli D., Boijunga N., Carninci P., de Bonaldo M.F.,
 RA: Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA: Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA: Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
 RA: Nordone P., Ring B., Rinewald M., Rodriguez I., Sakamoto N.,
 RA: Sasaki H., Sato K., Schoenbach C., Saya T., Shabata Y., Storch K.-P.,
 RA: Suzuki H., Toyoi-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA: Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
 RA: Hayashizaki Y.,

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GenCore version 5.1.3

• OX-2 membrane glycoprotein neural cell adhesion
 DM-GRASP Precurcassid
 neural cell adhesion molecule
 cell adhesion molecule
 cell adhesion molecule
 cell adhesion molecule
 carcinembryonic
 vacuolar cell adhesion
 neural cell adhesion
 cell surface glycans
 SHP substrate-1 F-actin
 ductal protein - m
 neural cell adhesion
 kinase-like protein

ALIGNMENTS

RESULT 1
 T08732
 hypothetical protein DKRZP566B0846.1 - human (fragment)

C.Species: Homo sapiens (man)

C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

R.Ottenwalder, B.; Obermaier, B.; Meves, H.W.; Gassnerhuber, J.; Wiemann, S.,
 submitted to the Protein Sequence Database, May 1999

A.Reference number: Z16474

A.Accession: T08732

A.Molecule type: mRNA

A.Residue: 1-407 <OT>

A.Cross-references: EMBL:AL050071

A.Experimental source: fetal kidney; clone DKRZP566B0846

C.Genetics:

C.Note: DKRZP566B0846.1

Query Match 50.4%; Score 1159.5; DB 2; Length 407;
 Best Local Similarity 70.3%; Pred. No. 9; 1e-78; 32; Indels 49; Gaps
 Matches 230; Conservative 16; Mismatches 32; Indels 49; Gaps

Qy 143 SGKVICKAVTPPLGNQSSTTVILVERPVLSLKGPSLSDIGGHEVIAICLNTGKVA 202
 Db 1 SGKVICKAVTPPLGNQSSTTVILVERPVLSLKGPSLSDIGGHEVIAICLNTGKVA 60

Qy 203 HIDEGDIDGEWSTTSFSPRETAITISQYKUPTRARRGRRITCIVKPALEDIRYSFI 262
 Db 61 HIDEGDIDGEWSTTSFSPRETAITISQYKUPTRARRGRRITCIVKPALEDIRYSFI 120

Qy 263 LDIOVAPLVSTGQDENWPRKGKVNLMKNAADANPPPKSVMWSLQGMPDGLASWTL 322
 Db 121 LDIOVAPEVSTGQDENWPRKGKVNLMKNAADANPPPKSVMWSLQGMPDGLASWTL 180

Qy 323 HFWPLTNTNSGVICKVMSLGSRSOKVYIISDWP----- 359
 Db 181 HFVHPPLTNTNSGVICKVMSLGSRSOKVYIISDWPPTTLQOPTIQWHIPSTDIEDLAT 240

Qy 360 -----PKTOSLILAVGAVGAVLAFIAITVLTLPKK-RPSYLDKV 403
 Db 241 ERPKKLPFPFLSTLAKDTATIATASVGGALPFLVLSVLGICFYRRRTFRGDYFAK- 299

Qy 404 IDLPLPHTRPPPLYERSSPPPLQKLO 430
 Db 300 -----NYIPPSDMOKES---QIDVQL 317

RESULT 2
 JC4024
 poliovirus receptor-related protein precursor - human
 C.Species: Homo sapiens (man)
 C.Date: 11-Jun-1995 #Sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C.Accession: JC4024

| | | | |
|--|--|---|--|
| | | Copyright (c) 1993 - 2002 Compugen Ltd. | Gencore version 5.1.3 |
| OM protein - protein search, using SW model | | | |
| Run on: | December 15, 2002, 09:39:57 ; Search time 21 Seconds | (without alignments) | 2513.228 Million cell updates/sec |
| Title: | US-09-972-268-4 | Sequence: | 1 MAMTPGPSLPGGSKAQLS EDDLVSHVGDGSVISRRRWYV 549 |
| Scoring table: | BLOSUM62 | Gapop: | 10.0 , Gapext: 0.5 |
| Searched: | 283224 seqs, 96134422 residues | Actual number of hits satisfying chosen parameters: | 283224 |
| Maximum DB seq length: | 0 | Maximum Match % | 100% |
| Post-processing: | Minimum Match 0% | Listing first 45 summaries | |
| Database : | PIR-73:* | | |
| | 1: pir1:* | | |
| | 2: pir2:* | | |
| | 3: pir3:* | | |
| | 4: pir4:* | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | |
| SUMMARIES | | | |
| Result No. | Score | Query Match % | Length DB ID |
| 1 | 2141 | 73.7 | 407 2 T08732 |
| 2 | 627 | 21.6 | 518 2 JC024 |
| 3 | 494 | 17.0 | 467 1 BLMP3 |
| 4 | 470 | 16.2 | A55437 |
| 5 | 463.5 | 16.0 | 478 2 A53950 |
| 6 | 449.5 | 15.5 | 538 2 I68093 |
| 7 | 422.5 | 14.5 | 417 2 A44194 |
| 8 | 415.5 | 14.3 | 392 2 B44194 |
| 9 | 390.5 | 13.4 | 392 1 RWIUPD |
| 10 | 390.5 | 13.4 | 417 1 RWIHPA |
| 11 | 331.5 | 11.4 | 416 2 A54017 |
| 12 | 230.5 | 7.9 | A43448 |
| 13 | 215.5 | 7.4 | 4391 2 A3095 |
| 14 | 201 | 6.9 | 5175 2 T28992 |
| 15 | 201 | 6.9 | 5198 2 T42290 |
| 16 | 198 | 6.8 | 588 2 JH0506 |
| 17 | 194 | 6.7 | 589 2 A45254 |
| 18 | 189 | 6.5 | 853 1 IUBNC |
| 19 | 187.5 | 6.5 | 273 2 A47639 |
| 20 | 187.5 | 6.5 | 7962 2 I3346 |
| 21 | 182 | 6.3 | JH0464 |
| 22 | 181.5 | 6.2 | 1896 2 TQ8851 |
| 23 | 179 | 6.2 | 3707 2 S1252 |
| 24 | 178.5 | 6.1 | 847 2 JH0171 |
| 25 | 174 | 6.0 | 858 1 IURNC |
| 26 | 173.5 | 6.0 | 761 1 IJHUNG |
| 27 | 173 | 5.9 | 637 2 B33785 |
| 28 | 172 | 5.9 | 513 2 JC5289 |
| 29 | 171.5 | 5.9 | 822 2 B49151 |
| ALIGNMENTS | | | |
| RESULT 1 | T08732 | Query Match % | 73.7%; Score 2141; DB 2; Length 407; |
| | | Best Local Similarity | 99.3%; Pred. No. 3.7e-145; |
| | | Matches | 494; Conservative 1; Mismatches 2; Indels 0; Gaps 0; |
| Qy | SGKVKICKAVTPIAGNAQSTTVVUVEPVLISLIKPSIDGNETVAIAKGPKA 202 | Db | 1 SGKVICKAVTPIAGNAQSTTVVUVEPVLISLIKPSIDGNETVAIAKGPKA 60 |
| Qy | 143 SGKVKICKAVTPIAGNAQSTTVVUVEPVLISLIKPSIDGNETVAIAKGPKA 202 | Db | 1 SGKVICKAVTPIAGNAQSTTVVUVEPVLISLIKPSIDGNETVAIAKGPKA 60 |
| Qy | 203 HIWEGDGEMESTTSFNETATISIQKLUFPTRARGRTTCVWHPALEKDRYSFI 262 | Db | 61 HIWEGDGEMESTTSFNETATISIQKLUFPTRARGRTTCVWHPALEKDRYSFI 120 |
| Qy | 263 LDQYQAYEPVSTGTDGNNVFGRGVNLCKNDAMPPEPESVRSRLQCPQDGLASDNTL 322 | Db | 121 LDQYQAYEPVSTGTDGNNVFGRGVNLCKNDAMPPEPESVRSRLQCPQDGLASDNTL 180 |
| Qy | 323 HFTPLILPNFNYGVYICKVUNSLQRQSKVYIISPPPTTQOPTLWHSTADELLAT 382 | Db | 181 HFTPLILPNFNYGVYICKVUNSLQRQSKVYIISPPPTTQOPTLWHSTADELLAT 240 |
| Qy | 383 ERKXKLPPLPLSTLAKDITATIASVGGLFLTVLVSIA3FCTERRERFRGQYAFN 442 | Db | 301 YIPSPDMQKESQIDVQDQBLDPYPPSVKRNKQFVNLRKQYLERPEKTOWNINLN 360 |
| Qy | 443 YIPSPDMQKESQIDVQDQBLDPYPPSVKRNKQFVNLRKQYLERPEKTOWNINLN 502 | Db | 503 RERPMQTYEIKMKNKFYSDTEIDEDDVLSHVDGSVISRRRWYV 549 |
| Qy | 503 RERPMQTYEIKMKNKFYSDTEIDEDDVLSHVDGSVISRRRWYV 549 | Db | 361 RERPMQTYEIKMKNKFYSDTEIDEDDVLSHVDGSVISRRRWYV 407 |
| RESULT 2 | JC4024 | | |



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OM protein - protein search, using sw model.

Run on: December 15, 2002, 09:04:27 ; Search time 14.5321 Seconds (without alignments)

Scoring table: BLOSUM62 US-09-972-268-8

Perfect score: 2679 Sequence: 1 PSPUCPGGKAKQLSASLIG..... KHHQNNDPKRKYIDPREHYV 504

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|--------|--------------------|-------|---|
| 1 | 1173.5 | 43.8 | 407 | T08732 hypothetical protein DKFP556B0846.1 - human (fragment) |
| 2 | 565.5 | 21.1 | 518 | JC4034 poliovirus receptor |
| 3 | 540 | 20.2 | 530 | A53437 poliovirus receptor |
| 4 | 527 | 19.7 | 538 | 168093 PR2 delta - human |
| 5 | 467 | 17.4 | 467 | 1 HLMSP3 poliovirus receptor |
| 6 | 455 | 17.0 | 478 | 2 I53960 PR2 alpha - human |
| 7 | 418 | 15.6 | 392 | B44194 poliovirus receptor |
| 8 | 418 | 15.6 | 417 | 2 A44194 poliovirus receptor |
| 9 | 402 | 15.0 | 392 | 1 RWHDUD poliovirus receptor |
| 10 | 402 | 15.0 | 417 | 1 RWHDUA poliovirus receptor |
| 11 | 326.5 | 12.2 | 416 | 2 A54017 colon carcinoma-as irregular chiasm C |
| 12 | 229.5 | 8.6 | 764 | A49448 perlecan precursor |
| 13 | 204.5 | 7.6 | 4391 | 2 A38036 hypothetical prote |
| 14 | 196.5 | 7.3 | 5175 | 2 T20992 hemicanthin precurs |
| 15 | 196.5 | 7.3 | 5198 | 2 T43290 OX-2 membrane glyc |
| 16 | 187.5 | 7.0 | 274 | 2 A47639 Down syndrome cell adhesion molecule |
| 17 | 181.5 | 6.8 | 1896 | 2 T08851 adhesion molecule surface glycoprote |
| 18 | 178 | 6.6 | 588 | 2 A45254 neural cell adhesi |
| 19 | 178 | 6.6 | 588 | 2 A45254 myelin-associated |
| 20 | 177.5 | 6.6 | 853 | 1 J1B0NC elastic titin - hu |
| 21 | 177 | 6.6 | 626 | 1 A61084 myelin-associated |
| 22 | 177 | 6.6 | 637 | 2 B33785 myelin-associated |
| 23 | 176 | 6.6 | 7962 | 2 138346 myelin-associated |
| 24 | 175 | 6.5 | 582 | 1 BNRT3 myelin-associated |
| 25 | 175 | 6.5 | 626 | 1 BNRT3 glial cell membran |
| 26 | 174 | 6.4 | 1091 | 2 AS8332 cexbaeke- and ade |
| 27 | 170.5 | 6.4 | 365 | 2 JC7780 heparan sulfate pr |
| 28 | 170.5 | 6.4 | 3707 | 2 S18352 B-cell adhesion pr |
| 29 | 164.5 | 6.1 | 847 | 2 JH0371 |

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

Query Match Score: 43.8%; Best Local Similarity: 62.8%; Pred. No. 4.5e-78; Matches: 240; Conservative: 28; Mismatches: 51; Indels: 63; Gaps: 7;

Db 1 SGKICKAVTFPLGNQSSITVVLVVEPTVILKPSDLSIDGNETTAICANGKPYA 196 QY 137 SGKICKAVTFPLGNQSSITVVLVVEPTVILKPSDLSIDGNETTAICANGKPYA 196

Db 1 SGKICKAVTFPLGNQSSITVVLVVEPTVILKPSDLSIDGNETTAICANGKPYA 60 QY 197 HIDEGDGEMESTS"SPFNETATISQYKUFPTRARERRITCWHPALEKDTRYSEI 256

Db 61 HIDEGDGEMESTS"SPFNETATISQYKUFPTRARERRITCWHPALEKDTRYSEI 120 QY 257 LDIVIAPESVYGVQDNWFGRKVKVNMKCNADANPPVSKWMLDQWPGQLLASNTL 316

Db 121 LDIVIAPESVYGVQDNWFGRKVKVNMKCNADANPPVSKWMLDQWPGQLLASNTL 180 QY 317 HFVPLTNTNSVYVCKVNTSLQRSPDKVYTSIP----- 353

Db 181 HFVPLTNTNSVYVCKVNTSLQRSPDKVYTSIP----- 240 QY 354 -----FQKOTSIAYAGAVIGAVIAALTTIAFVFTWLTHTRKK--RPSYLDKV 397

Db 241 EPKLQLPFLSTIATKDDITATIASVGGALPITVNLVSLAGFCYKRRFRGQYPAQI 300 QY 398 IDLUPTH-----KPPPLYEERSSPPLQFDLFOPEHL--PLQTOFKEERVG 440

Db 301 Y-PPSDMQKSSQIQVLQQDRLDPYPSVKGENKNPVNNLIRKDLBSEPTKVN---N 354 QY 441 NLSQSNGLNSSFDFDDEPDENFGV 462

Db 355 NVENLNRF-ERPMQTYEDLKG 375

RESULT 2

JC4024

| | | | | | | | |
|---------------------------|---|---|------|-----|-----|---|-----|
| Qy | 121 | VLFKNYSLNDATITLNGPFDSDKTYCKATVTPLOAQSSTTITUVEPTISLKGPSD | 180 | Qy | 61 | IVEPVIAWGVNSLKCLIEVNFTIISWEKLHRSSTOVAVRHPQGFSVQGEYQGR | 120 |
| Db | 121 | VLFKNYSLNDATITLNGPFDSDKTYCKATVTPLOAQSSTTIVLVEPTISLKGPSD | 180 | Db | 61 | IVEPVIAWGVNSLKCLIEVNFTIISWEKLHRSSTOVAVRHPQGFSVQGEYQGR | 120 |
| Qy | 181 | LDDGGNETVAICILATEKPVANIDWEDLGEMESTTIFPNETATISQYKLFTRFAR | 240 | Qy | 121 | VLFKNYSLNDATITLNGPFDSDKRYCKATVTPLOAQSSTTIVLVEPTISLKGPSD | 180 |
| Db | 181 | LDDGGNETVAICILATEKPVANIDWEDLGEMESTTIFPNETATISQYKLFTRFAR | 240 | Db | 121 | VLFKNYSLNDATITLNGPFDSDKRYCKATVTPLOAQSSTTIVLVEPTISLKGPSD | 180 |
| Qy | 241 | GRRITCVVKPALEKDIRYSPIDIOVAPESVTGDNWPKRGWYCKTNLSLGQSDQKVYISDPT | 300 | Qy | 181 | LIDGGNETVAAICIACTGPKVANIDWEDLGEMESTTIFPNETATISQYKLFTRFAR | 240 |
| Db | 241 | GRRITCVVKPALEKDIRYSPIDIOVAPESVTGDNWPKRGWYCKTNLSLGQSDQKVYISDPT | 300 | Db | 181 | LIDGGNETVAAICIACTGPKVANIDWEDLGEMESTTIFPNETATISQYKLFTRFAR | 240 |
| Qy | 301 | KSWWSRLDGWPDGILASNTLHFVPLTENYSGVYICKTNLSLGQSDQKVYISDPT | 360 | Qy | 241 | GRRITCVVKPALEKDIRYSPIDIOVAPESVTGDNWPKRGWYCKTNLSLGQSDQKVYISDPT | 300 |
| Db | 301 | KSWWSRLDGWPDGILASNTLHFVPLTENYSGVYICKTNLSLGQSDQKVYISDPT | 360 | Db | 241 | GRRITCVVKPALEKDIRYSPIDIOVAPESVTGDNWPKRGWYCKTNLSLGQSDQKVYISDPT | 300 |
| Qy | 361 | TTLQOPTIQWHPSTADIEDATEPKCLPFPPLSTLKDITATIASVVGALFIVLVS | 420 | Qy | 301 | KSWWSRLDGWPDGILASNTLHFVPLTENYSGVYICKTNLSLGQSDQKVYISDPT | 360 |
| Db | 361 | TTLQOPTIQWHPSTADIEDATEPKCLPFPPLSTLKDITATIASVVGALFIVLVS | 420 | Db | 301 | KSWWSRLDGWPDGILASNTLHFVPLTENYSGVYICKTNLSLGQSDQKVYISDPT | 360 |
| Qy | 421 | VLAGIFCYRRETFRGDYFKNYIPPSDQMOKESQIDVLOQEDPSYPSVKCENKPNVN | 480 | Qy | 361 | TTLQOPTIQWHPSTADIEDATEPKCLPFPPLSTLKDITATIASVVGALFIVLVS | 420 |
| Db | 421 | VLAGIFCYRRETFRGDYFKNYIPPSDQMOKESQIDVLOQEDPSYPSVKCENKPNVN | 480 | Db | 361 | TTLQOPTIQWHPSTADIEDATEPKCLPFPPLSTLKDITATIASVVGALFIVLVS | 420 |
| Qy | 481 | LIRKDYLEEPEKTONVNENLNRFERMDYEDLDRGMKPFVSEHYDENEDDLVSHVDGS | 540 | Qy | 421 | VLAGIFCYRRETFRGDYFKNYIPPSDQMOKESQIDVLOQEDPSYPSVKCENKPNVN | 480 |
| Db | 481 | LIRKDYLEEPEKTONVNENLNRFERMDYEDLDRGMKPFVSEHYDENEDDLVSHVDGS | 540 | Db | 421 | VLAGIFCYRRETFRGDYFKNYIPPSDQMOKESQIDVLOQEDPSYPSVKCENKPNVN | 480 |
| Qy | 541 | VISREVVV 549 | | Qy | 481 | LIRKDYLEEPEKTONVNENLNRFERMDYEDLDRGMKPFVSEHYDENEDDLVSHVDGS | 540 |
| Db | 541 | VISREVVV 549 | | Db | 481 | LIRKDYLEEPEKTONVNENLNRFERMDYEDLDRGMKPFVSEHYDENEDDLVSHVDGS | 540 |
| | | | | Qy | 541 | VISREVVV 549 | |
| | | | | Db | 541 | VISREVVV 549 | |
| RESULT 2 | | | | | | | |
| Q9JLB9 | | PRELIMINARY; | PRT; | 549 | AA. | | |
| ID | Q9JLB9; | | | | | | |
| AC | Q9JLB9; | | | | | | |
| DT | 01-OCT-2000 (T-TMBLrel. 15, Created) | | | | | | |
| DT | 01-OCT-2000 (T-TMBLrel. 15, Last sequence update) | | | | | | |
| DT | 01-DEC-2001 (T-TMBLrel. 19, Last annotation update) | | | | | | |
| DE | Cell adhesion molecule nectin-3 alpha. | | | | | | |
| GN | PRVL3 | | | | | | |
| OS | Mus musculus (Mouse) | | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutherzia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; | | | | | | |
| OX | [1] | | | | | | |
| RP | SEQUENCE FROM N.A. MEDLINE=2009443; PubMed=10744716; RA | | | | | | |
| RX | RA | | | | | | |
| RA | Sach-Horikawa K., Nakaniishi H., Takahashi K., Miyahara M., Tachibana K., Mizoguchi A., Takai Y.; RT | | | | | | |
| RT | that shows homophilic and heterophilic cell-cell adhesion activities."; Nectin-3: a new member of immunoglobulin-like cell adhesion molecules | | | | | | |
| RT | InterPro; IPR003599; Ig-like. InterPro; IPR003606; Ig_MHC. InterPro; IPR003006; Ig_MHC. Pfam; PF00047; Ig_1. SMART; SM00409; Ig_1. SMART; SM00410; Ig_1-like; 1. DR | | | | | | |
| DR | MCDB; MGI:1530171; Pvr133. | | | | | | |
| DR | IPR003833; AAFAF3685; 1; -. | | | | | | |
| DR | IPR00047; Ig_2. | | | | | | |
| DR | SMART; SM00409; Ig_1. | | | | | | |
| DR | SMART; SM00410; Ig_1-like; 1. | | | | | | |
| SQ | SEQUENCE 549 AA; 6083 MW; 549C9ABB47F185 CRC64; | | | | | | |
| Query Match | 91.3%; Score 2739; DB 11; Length 549; | | | | | | |
| Best Local Similarity | 93.3%; Pred. No. 5-3e-207; | | | | | | |
| Matches 512; Conservative | 19; Mismatches 18; Indels 0; Gaps 0; | | | | | | |
| Qy | 1 MARTGPSPICPGGGKAQISSASLLGAGLILQPPTPPPLLLFPLLFSLRCGALAGPI 60 | | | | | | |
| Db | 1 MARTGPSPICPGGGKAQISSASLLGAGLILQPPTPPPLLLFPLLFSLRCGALAGPI 60 | | | | | | |